Serial Number: 09/841,963 A

CRF Processing Date: 2/21/2002
Edited by: _____
Verified by: _____ (STIC staff)

ENTERED

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#8/Raw Seq. Listing

- ☐ Changed a file from non-ASCII to ASCII

- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- ☐ Edited a format error in the Current Application Data section, specifically:
  _____

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
  _____

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
  _____

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
  _____

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included: .

- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
  _____

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

- ☐ Inserted mandatory headings, specifically: _____

- ☑ Corrected an obvious error in the response, specifically:
  <1507 response

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically:
  _____

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- ☐ Other:
  _____
  _____
  _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

1600

RAW SEQUENCE LISTING   DATE: 02/21/2002
PATENT APPLICATION: US/09/841,963A   TIME: 22:29:38

Input Set : N:\Crf3\02132002\I841963A.raw
Output Set: N:\CRF3\02212002\I841963A.raw

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 1 <110> APPLICANT: Watson, Dennis K.
 2        Papas, Takis S. (Deceased)
 3        Papas, Tula C. (Legal Representative)
 4 <120> TITLE OF INVENTION: Methods and compositions for the diagnosis and
 5        treatment of cancer
 6        based on transcription factor ETS2
 7 <130> FILE REFERENCE: 10545-015-999
 8 <140> CURRENT APPLICATION NUMBER: US/09/841,963A
 9 <141> CURRENT FILING DATE: 2001-04-25
10 <150> PRIOR APPLICATION NUMBER: PCT/US99/27805
11 <151> PRIOR FILING DATE: 1999-11-23
12 <150> PRIOR APPLICATION NUMBER: 60/109,850
13 <151> PRIOR FILING DATE: 1998-11-25
14 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: PatentIn version 3.0
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18 <211> LENGTH: 1894
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
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23 <222> LOCATION: (416)..(1423)
24 <400> SEQUENCE: 1
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27     ccagcaggca gccctgggct gggggtaggg gactccctac aggcacgcag ccctgagacc     180
28     gccaccagcc accccttgag ggtggccagg cccccagtgg ccaacctgag tgctgcctct     240
29     gccaccagcc ctgctggccc ctggttccgc tggcccccca gatgcctggc tgagacacgc     300
30     cagtggcctc agctgcccac acctcttccc ggcccctgga gttggcactg cagcagacag     360
31     ctccctgggc accaggcagc taacagacac agccgccagc ccaaacagca gcggc atg     418
32                                                                 Met
33                                                                   1
34     ggc agc gcc agc ccg ggt ctg agc agc gta tcc ccc agc cac ctc ctg     466
35     Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu Leu
36                 5                  10                  15
37     ctg ccc ccc gac acg gtg tcg cgg aca ggc ttg gag aag gcg gca gcg     514
38     Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala Ala
39              20                  25                  30
40     ggg gca gtg ggt ctc gag aga cgg gac tgg agt ccc agt cca ccc gcc     562
41     Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro Ala
42          35                  40                  45
43     acg ccc gag cag ggc ctg tcc gcc ttc gac ctc tcc tac ttt gac atg     610
44     Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp Met
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RAW SEQUENCE LISTING   DATE: 02/21/2002
PATENT APPLICATION: US/09/841,963A   TIME: 22:29:38

Input Set : N:\Crf3\02132002\I841963A.raw
Output Set: N:\CRF3\02212002\I841963A.raw

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47     Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala Ser
48                           70                    75                    80
49     agt cgg gag gag cca cct gac cag cct gag cag tgc ccg gtc att gac       706
50     Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile Asp
51                           85                    90                    95
52     agc caa gcc cca gcg ggc acc ctg gac ttg gtg ccc ggc ggg ctg acc       754
53     Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu Thr
54                           100                   105                   110
55     ttg gag gag cac tcg ctg gag cag gtg cag tcc atg gtg gtg ggc gaa       802
56     Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly Glu
57                115                   120                   125
58     gtg ctc aag gac atc gag acg gcc tgc aag ctg ctc aac atc acc gca       850
59     Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr Ala
60     130                   135                   140                   145
61     gat ccc atg gac tgg agc ccc agc aat gtg cag aag tgg ctc ctg tgg       898
62     Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu Trp
63                           150                   155                   160
64     aca gag cac caa tac cgg ctg ccc ccc atg ggc aag gcc ttc cag gag       946
65     Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln Glu
66                165                   170                   175
67     ctg gcg ggc aag gag ctg tgc gcc atg tcg gag gag cag ttc cgc cag       994
68     Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg Gln
69                180                   185                   190
70     cgc tcg ccc ctg ggt ggg gat gtg ctg cac gcc cac ctg gac atc tgg      1042
71     Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile Trp
72                195                   200                   205
73     aag tca gcg gcc tgg atg aaa gag cgg act tca cct ggg gcg att cac      1090
74     Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile His
75     210                   215                   220                   225
76     tac tgt gcc tcg acc agt gag gag agc tgg acc gac agc gag gtg gac      1138
77     Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val Asp
78                           230                   235                   240
79     tca tca tgc tcc ggg cag ccc atc cac ctg tgg cag ttc ctc aag gag      1186
80     Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys Glu
81                245                   250                   255
82     ttg cta ctc aag ccc cac agc tat ggc cgc ttc att agg tgg ctc aac      1234
83     Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu Asn
84                260                   265                   270
85     aag gag aag ggc atc ttc aaa att gag gac tca gcc cag gtg gcc cgg      1282
86     Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg
87                275                   280                   285
88     ctg tgg ggc atc cgc aag aac cgt ccc gcc atg aac tgc gac aag ctg      1330
89     Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys Leu
90     290                   295                   300                   305
91     agc cgc tcc atc cgc cag tct tac aag aag ggc atc atc cgg aag cca      1378
92     Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys Pro
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97      gtgcctggcc caggggcctga aacccgcccct caggggcctc tctcctgcct gccctgcctc    1483
98      agccaggccc tgagatgggg gaaaacgggc agtgtgctct gctgctctga ccttccagag    1543
99      cccaaggtca gggaggggca accaactgcc ccagggggat atgggtcctc tggggccttc    1603
100     gggaccatgg ggcaggggtg cttcctcctc aggcccagct gctccctgg aggacagagg     1663
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103     ctgcctccca ttctgcacca cacctggcat ggtgcaggga gacatctgca cccctcagtt     1843
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108 <212> TYPE: PRT
109 <213> ORGANISM: Homo sapiens
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114                 20                  25                  30
115     Ala Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro
116                 35                  40                  45
117     Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp
118             50                  55                  60
119     Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala
120     65                  70                  75                  80
121     Ser Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile
122                 85                  90                  95
123     Asp Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu
124                 100                 105                 110
125     Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly
126             115                 120                 125
127     Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr
128             130                 135                 140
129     Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu
130     145                 150                 155                 160
131     Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln
132                 165                 170                 175
133     Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg
134             180                 185                 190
135     Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile
136             195                 200                 205
137     Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile
138         210                 215                 220
139     His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val
140     225                 230                 235                 240
141     Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys
142                 245                 250                 255
143     Glu Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu
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144                    260              265              270
145      Asn Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala
146             275              280              285
147      Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys
148             290              295              300
149      Leu Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys
150      305              310              315              320
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155 <211> LENGTH: 1704
156 <212> TYPE: DNA
157 <213> ORGANISM: Mus sp.
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159 <221> NAME/KEY: CDS
160 <222> LOCATION: (362)..(1336)
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164      tagacctgca ggcctgaggc ctcagactca cactcaaggg gcaagaggcc ctggtggccc   180
165      acctaagagc cacctctgtc cccagccctg ctgccccact gatgtctgac tgagacccag   240
166      cagtgaccct gagctgcctg cccactgcct cctcctggtc cctgaggttg gctctgccga   300
167      ggacggacga tctcttctgaa gcaggcggct aacggaagca gccccaagcc tccaccgcag   360
168      c atg ggc agt gcc agc cca ggc ctg agc aac gtg tcc ccc ggt tgc ctg   409
169        Met Gly Ser Ala Ser Pro Gly Leu Ser Asn Val Ser Pro Gly Cys Leu
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171      cta ctg ttc cca gat gtg gca cca cga aca ggg acg gag aag gca gca      457
172      Leu Leu Phe Pro Asp Val Ala Pro Arg Thr Gly Thr Glu Lys Ala Ala
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174      tca gga gca atg ggc cct gag aag cag gaa tgg agt cct agt cca ccc      505
175      Ser Gly Ala Met Gly Pro Glu Lys Gln Glu Trp Ser Pro Ser Pro
176             35               40               45
177      gcc acc cct gag cag ggc ctg tct gct ttc tac ctc tct tac ttt aac      553
178      Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asn
179             50               55               60
180      atg tat ccc gac gat agc agc tgg gtc gcc aaa gtc ccc gag gcc cgt      601
181      Met Tyr Pro Asp Asp Ser Ser Trp Val Ala Lys Val Pro Glu Ala Arg
182      65               70               75               80
183      gcc ggg gag gac cac ccg gag gag ccc gag cag tgt ccc gtc att gac      649
184      Ala Gly Glu Asp His Pro Glu Glu Pro Glu Gln Cys Pro Val Ile Asp
185                      85               90               95
186      agc cag gcc tct ggg agc acg ttg gat gag cac tcg cta gag cag gtg      697
187      Ser Gln Ala Ser Gly Ser Thr Leu Asp Glu His Ser Leu Glu Gln Val
188             100              105              110
189      caa tcg atg gtt gtg ggc gag gtc ctg aaa gat att gag acg gcc tgc      745
190      Gln Ser Met Val Val Gly Glu Val Leu Lys Asp Ile Glu Thr Ala Cys
191             115              120              125
192      aag ctt gtg aac atc aca gca gac cct ggg gac tgg agc cct ggt aac      793
193      Lys Leu Val Asn Ile Thr Ala Asp Pro Gly Asp Trp Ser Pro Gly Asn
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201          tcc gag gaa cag ttc cgt cag cgt gca ccc ttg ggt ggg gat gta ctg      937
202          Ser Glu Glu Gln Phe Arg Gln Arg Ala Pro Leu Gly Gly Asp Val Leu
203                       180               185               190
204          cat gcc cac ctg gac atc tgg aag tca gcg gcc tgg atg aag gag agg      985
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206                   195               200               205
207          acc tcg cct ggg acc ctt cac tac tgc gcc tcc acc agc gag gac ggc      1033
208          Thr Ser Pro Gly Thr Leu His Tyr Cys Ala Ser Thr Ser Glu Asp Gly
209              210               215               220
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211          Trp Thr Asp Gly Glu Val Asp Ser Ser Cys Ser Gly Gln Pro Ile His
212          225               230               235               240
213          ctg tgg cag ttc ctg aaa gaa ctg ctg ctc aag ccc cac agc tat ggc      1129
214          Leu Trp Gln Phe Leu Lys Glu Leu Leu Leu Lys Pro His Ser Tyr Gly
215                           245               250               255
216          cgc ttc atc cgg tgg ggt gtg cgc aag aac cgg cca gcc atg aac tat      1177
217          Arg Phe Ile Arg Trp Gly Val Arg Lys Asn Arg Pro Ala Met Asn Tyr
218                       260               265               270
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226          Lys Gly Met Ile Arg Lys Pro Ala Ile Ser Gln Arg Leu Val Tyr Gln
227          305               310               315               320
228          ttt gtg cat cca gtc tgagagccac agagaccaga ggcctacaac ctgccccagg      1376
229          Phe Val His Pro Val
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232          tcccagaacc caaggtccca gatagacagc cactgatcta cccatacaca tgagctctct      1496
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VERIFICATION SUMMARY   DATE: 02/21/2002
PATENT APPLICATION: US/09/841,963A TIME: 22:29:39

Input Set : **N:\Crf3\02132002\I841963A.raw**
Output Set: **N:\CRF3\02212002\I841963A.raw**

L:8 M:270 C: Current Application Number differs, Wrong Format